



RAW SEQUENCE LISTING ERROR REPORT

JUL 20 2004

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/762,283
Source: 1600
Date Processed by STIC: 7/7/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM; ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

International Division
Legal Staff

- 2 JUL 2004

RECEIVED

BEST AVAILABLE COPY

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/762,283

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO: X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences
- 8 ☐ Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000
- 9 ☐ Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>.<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC - Biotechnology Systems Branch - 09/09/2003

BEST AVAILABLE COPY



1600

RAW SEQUENCE LISTING

DATE: 07/07/2004

PATENT APPLICATION: US/09/762,283

TIME: 15:43:25

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\07072004\I762283.raw

3 <110> APPLICANT: Perez Gomariz, Rosa
 4 Leceta Martinez, Javier
 5 Delgado Mora, Mario
 6 Martinez Mora, Carmen
 8 <120> TITLE OF INVENTION: Method for Treating Endotoxic Shock and Inflammatory and Autoimmune
 9 Diseases in Mammals
 W--> 10 <130> FILE REFERENCE: 100700-09144 [HERR 18.313]
 12 <140> CURRENT APPLICATION NUMBER: US 09/762,283
 C--> 14 <141> CURRENT FILING DATE: 2001-03-28
 16 <160> NUMBER OF SEQ ID NOS: 3

ERRORED SEQUENCES

18 <210> SEQ ID NO: 1
 20 <211> LENGTH: 28
 22 <212> TYPE: PRT
 24 <213> ORGANISM: Homo sapiens
 26 <400> SEQUENCE: 1
 E--> 28 His Ser Asp Ala Val Phe Thr Asp Asn Tyr Thr
 29 1 5 5 10 10
 31 Arg Leu Arg Lys Gln Met Ala Val Lys Lys Tyr
 E--> 32 15 20 15 20
 34 Leu Asn Ser Ile Leu Asn NH2
 E--> 35 25 25
 37 <210> SEQ ID NO: 2
 39 <211> LENGTH: 28
 41 <212> TYPE: PRT
 43 <213> ORGANISM: Homo sapiens
 45 <400> SEQUENCE: 2
 E--> 47 His Ser Asp Gly Ile Phe Thr Asp Ser Tyr Ser Arg Tyr
 48 1 5 10 5 10
 E--> 50 Arg Lys Gln Met Ala Val Lys Lys Thy Leu Ala Ala Val
 E--> 51 15 20 25 20
 53 Leu Gly Lys Arg Tyr Lys Gln Arg Val Lys Asp Lys NH2
 E--> 54 30 28 35 30 35
 56 <210> SEQ ID NO: 3
 58 <211> LENGTH: 26
 60 <212> TYPE: PRT
 62 <213> ORGANISM: Homo sapiens
 64 <400> SEQUENCE: 3
 E--> 66 His Ser Asp Gly Ile Phe Thr Asp Ser Tyr Ser Arg Tyr
 67 1 5 10 10

Does Not Comply
 Corrected Diskette Needed

Summary sheet. (ps. 1-3)

Invalid Amino
 Acid

p/s see item
 # 3 on page
 summary sheet.

delete

same
 error

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/762,283

DATE: 07/07/2004

TIME: 15:43:25

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\07072004\I762283.raw

E--> 69 Arg Lys Gln Met Ala Val Lys Lys Thy Leu Ala Ala Val
E--> 70 15 26 25 20
72 Leu NH2

delete

*Invalid
Amino
Acid*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/762,283

DATE: 07/07/2004

TIME: 15:43:26

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\07072004\I762283.raw

L:10 M:283 W: Missing Blank Line separator, <130> field identifier
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:29 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1 ✓
M:332 Repeated in SeqNo=1
L:35 M:252 E: No. of Seq. differs, <211> LENGTH:Input:28 Found:22 SEQ:1 ✓
L:48 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2 ✓
L:50 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1 ✓
M:332 Repeated in SeqNo=2
L:54 M:252 E: No. of Seq. differs, <211> LENGTH:Input:28 Found:26 SEQ:2 ✓
L:67 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3 ✓
L:69 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1 ✓
M:332 Repeated in SeqNo=3